

104007" 46502660

<sup>EcoRI</sup>  
AGTGAATTC CGATAG TTCAATTGT TAAAGACAGG ATCTCAGTAG 7740  
TCCAGGCTTT AGTCTGACT CAACAATACC ACCAGCTAAA ACCACTAGAA TACGAGCCAC 7800  
AATAATATAA AGATTTTATT TAGTTTCCAG AAAAAGGGGG <sup>IR</sup> GAATGAAAGA CCCCACCAAA 7860  
REFMLVCGD. ENV  
TTGCTTAGCC TGATAGCCGC AGTAAAGCCA TTTTGCAAGG CATGGAAAA TACCAAAACA 7920  
AGAATAGAGA AGTTCAGATC AAGGGGGGGT ACACGAAAC AGCTAACGTT GGGCCAAACA 7980  
GGATATCTGC GGTGAGCAGT TTCGGCCCCG GCCCGGGGCC AAGAACAGAT GGTACACCGG 8040  
GTTCCGCCCC GCGCCGGGGC CAAGAACAGA TGCTCCCCAG ATATGGCCCA ACCCTCAGCA 8100  
GTTTCTTAAG ACCCATCAGA TGTCTCCAGG CTCCCCCAAG GACCTGAAT GACCTGTGC 8160  
CTTATTGAA TTAACCAATC AGCTGTCTC TCGTTCTGT TCGCGCGCTT CTGCTTCCC 8220  
AGCTCTATAA AAGAGCTCAG AACCCTCAC <sup>U3</sup> <sup>KpnI</sup>  
GGCCAGTCC TCCGATAGAC TGAGTCGCC <sup>SmaI</sup> GGTACCCGT GTATCAATA AATCCTCTG 60  
CTGTTGCATC CGACTCGTG <sup>IR</sup> CCTTGGGAGG GTCTCTCAG AGTGATTGAC 120  
TACCCGTCTC GGGGTCTTT CATTTGGGG CTCGTCCGG ATCTGGAGAC CCCTGCCAC 180  
GGACCACCGA CCCACCACCG GGAGGTAAAG TGGCCAGCAA TTGTTCTGT TCTGTCCATT 240  
GTCCTGTGTC TTGATTGAT TTTATGCGC TGTGTCTGTA <sup>SplI</sup> CTAGTTGGCC GACTAGATTG 300

FIGURE 1a

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Bam HI → Pst I GCSA  
 GTATCTGGCG GATCCGTGGT GGAAGTGAAG AGTTGAGAC ACCCGGCGC AACCTGGGA 360  
 GAGCTCCAG GGACTTCGGG GGCCATTTT GTGGCCCGG CAGAGTCAA CCATCCCGAT 420  
 CGTTTGGAC TCCTTGGTGC ACCCCCTTA GAGGAGGGT ATGTGTTCT GGTAGGAGAC 480  
 AGAGGGCTAA AACGGTTTC GCCCGGTCT GAGTTTTCG TTTCTGTTG GAACCGAAGC 540  
 CGCGCCGCGC GTCTGTCTG [H<sub>1</sub>I] GTCTGTGTT GACTGTTTT 600  
 CTGTATTGT CTGAAACAT → 909 GTTCTGTTT GACTGTTTT 600  
 CACTGGAAG ATGTGAACG REFMLVCGH.GAG H<sub>1</sub>P 15 GACTTTAGAC 660  
 TGGGTTACAT TCTGCTCTGC AGAATGGCCA ACCTTCAACG TGGATGGCC ACGAGACGGC 780  
 ACTTTTAACC CAGACATTAT TACACAGGT AAGATCAAGG TCTTCTCACC TGGCCACAT 840  
 GGACATCCGG ATCAGGTCCC CTACATCGTG ACCTGGGAAG CTATAGCAGT AGACCCCTCT 900  
 CCCTGGGTCA GACCCCTCGT GCACCCTAA CCTCCCTCT CTCTTCCCGC TTCAGCCCCC 960  
 TCTCTCCAC CTGAACCCCG ACTCTCGACC CCGCCCGAGT CCTCCCTCTA TCGGGCTCTC 1020  
 ACTTCTCCTT TAACACACCA ACCTAGGCCT [H<sub>1</sub>I] CAAGTCCTTC CTGATAGCGG AGGACCCTC 1080

FIGURE 1b

FIGURE 1c

ATTGATCTAC TCACGGAGGA CCTCCGCCT TACCGGGACC CAGGGCCACC CTCTCTGAC 1140  
GGGAACGGCG ATAGCGGAGA AGTGGCCCTT ACAGAAGGAG CCCCTGACCC TTCCCCAATG 1200  
GTATCCGCC TCGGGGAG AAAGAACC CCCGTGGCG ATTCTACTAC CTCTCAGGCG 1260  
TTCCCCCTC GCCTGGGAG GAATGGACAG TATCAATACT GGCCATTTTC CTCTCTGAC 1320  
CTCTATAACT GGAATAATA CAACCCCTCT TTCTCCGAGG ACCCAGCTAA ATTGACAGCT 1380  
TTCATCGAGT CCGTCTCTT TACTCATCAG CCCACTTGGG ATGACTGCCA ACAGCTATTA 1440  
GGGACCTGC TGACGGGAGA AGAANAACAG CGAGTGCTCC TAGAGGCCCG AAAGCGGTT 1500  
CGAGGGGAGG ACGGACGCC AACTCAG GGGATCCTCTAGAGTCGACCTGCATGCAAGCT  
BamHI XbaI PstI HindII SphI  
SalI HincII AccI  
CAGATCCCAT TCGATTAG TTCAATTGT TAAAGACAGG ATCTCAGTAG 7740  
TCCAGGCTTT AGTCCTGACT CAACAATACC ACCAGCTAAA ACCACTAGAA TAGGAGCCAC 7800  
AATAATATAA AGATTTTATT TAGTTTCCAG AAAAAGGGGG GAATGAAGA CCCCACCAAA 7860  
REFMLVCGD. ENV<

FIGURE 1c

TTGCTTAGCC TGATAGCGC AGTAACGCCA TTTTGCAAG CATGAAAAA TACCAAACCA 7920  
AGAATAGACA AGITCAGATC AAGGGCGGT ACACGAAAC AGCTAACGTT GGGCCAAAACA 7980  
GGATATCTGC GGTGAGCAGT TTCGGCCCCG GCCCGGGGC AAGAACAGAT GTTCACCGCG 8040  
GTTCGGCCCC GGCCCGGGGC CAAGAACHGA TGGTCCCCAG ATATGGCCCA ACCCTCAGCA 8100  
GTTTCTTAAG ACCCATCAGA TGTTTTCCAG CTCCCCCAAG GACCTGAAAT GACCCTGTGC 8160  
CTTATTGAA TTAAACCAATC AGCCTGCTTC TCGTTCTGT TCGCGCGCT CTGCTTCCC 8220  
AGCTCTATAA AAGAGCTCAC AACCCCTCAC

Annotations:  
 $\rightarrow R$   
 $\xrightarrow{U_5}$   
 $\xrightarrow{S_{NAI}}$   
 $\xrightarrow{K_n L_7}$   
 $\xleftarrow{U_3}$   
 $\xrightarrow{P_R S}$   
 $\xrightarrow{S_D}$   
 $\xrightarrow{PUC 19}$

FIGURE 1d

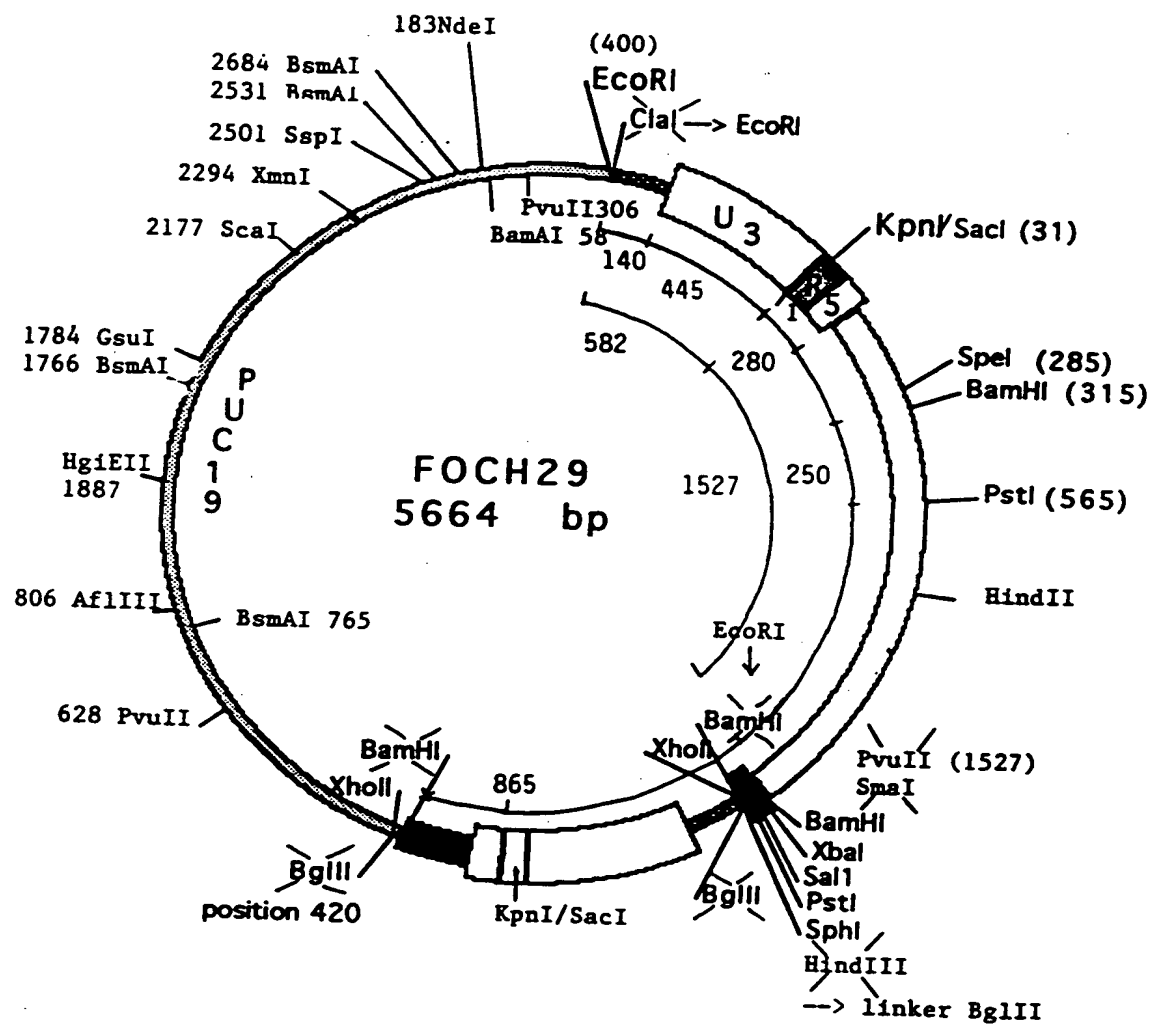
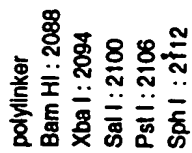


FIGURE 2 A

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**FIGURE 2B**

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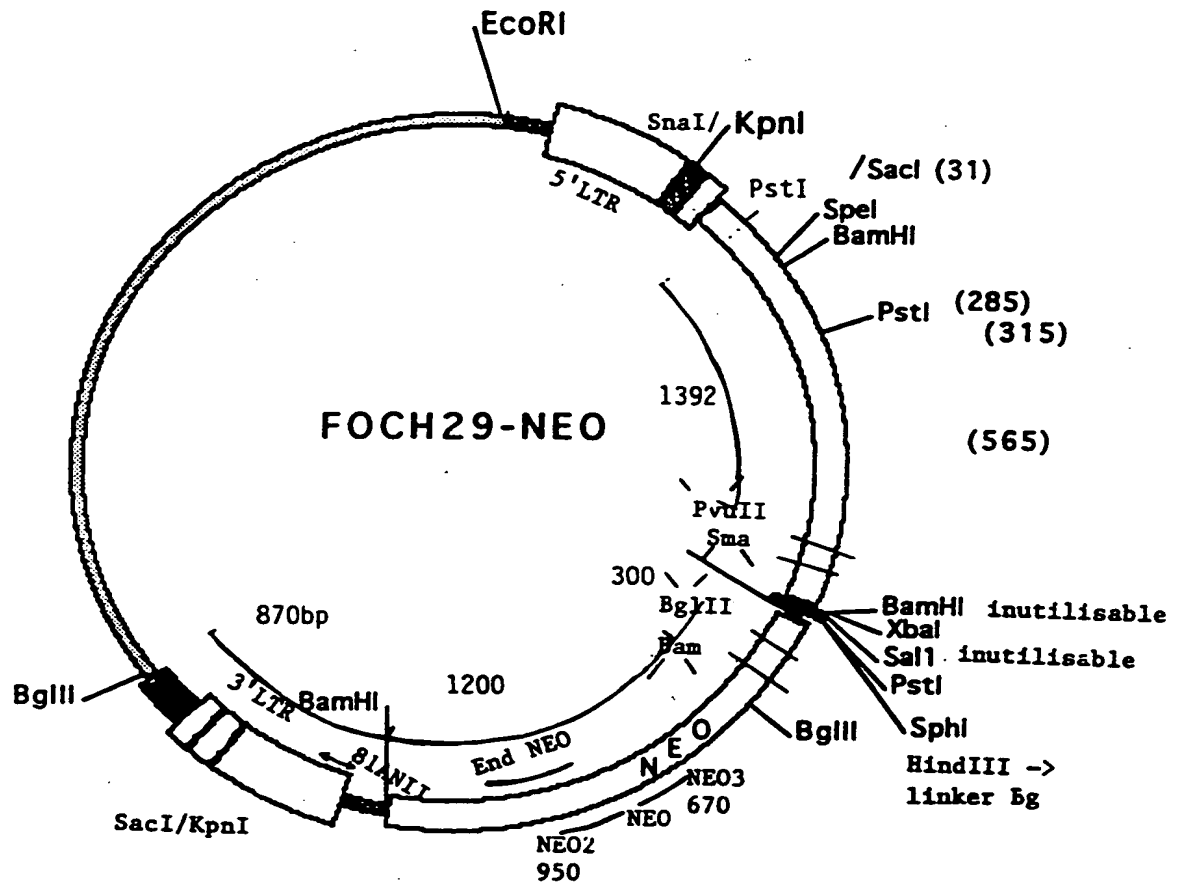
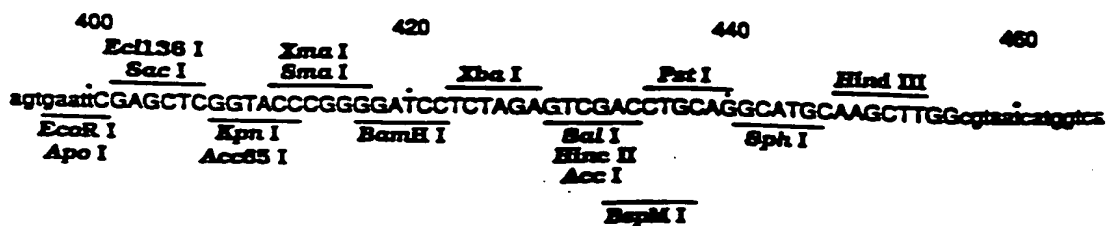
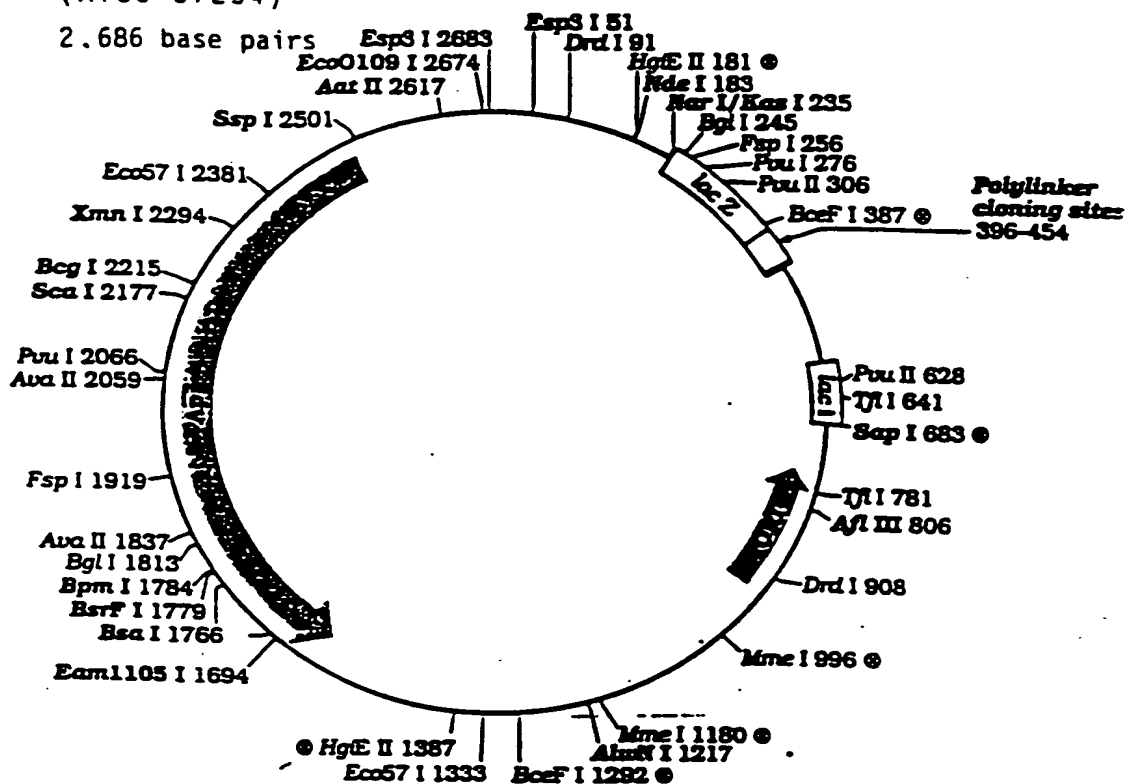


FIGURE 3

pUC19  
 (ATCC 37254)

2.686 base pairs



*LacZ*—Ala Leu Ser Asn Ser Ser Pro Val Arg Pro Asp Glu Leu Thr Ser Arg Cys Ala His Leu Ser Pro Thr Ile Met Thr

#### References

1. Yanisch-Perron, C., Vieira, J. and Messing, J. (1985) *Gene* 33, 103-119.
2. Genbank Accession # V80026 (Vector:pUC19c).

FIGURE 4



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R  
KpnI  
SmaI  
U5  
TR  
PBS  
SD  
SpeI  
BamHI  
Pr75 GCSA  
PstI  
gus  
REFMLVGD.GAG  
Map15  
Map15  
pp12  
StuI  
p12  
CAp30  
début FMS15 1447-1468  
PvuII  
(1527)  
N+B+

GCGCCAGTCC TCCGATAGAC TGAGTCGCCC GGGTACCCGT GTATCCAATA AATCCTCTTG 60  
CTGTTGCATC CGACTCGTGG TCTCGCTGTT CCTTGGGAGG GTCTCCTCAG AGTGATTGAC 120  
TACCCGTCTC GGGGGTCTTT CATTTGGGGG CTCGTCCGGG ATCTGGAGAC CCCTGCCCAG 180  
GGACCACCGA CCCACCACCG GGAGGTAAGC TGGCCAGCAA TTGTTCTGTG TCTGTCCATT 240  
GTCCTGTGTC TTTGATTGAT TTTATGCGCC TGTGTCTGTA CTAGTTGGCC GACTAGATTG 300  
GTATCTGGCG GATCCGTGGT GGAAGTACG AGTTCGAGAC ACCCGGCCGC AACCCCTGGGA 360  
GACGTCCCAG GGAAGTCCGG GGCATTTTT GTGGCCCGGC CAGAGTCCAA CCATCCCGAT 420  
CGTTTTGGAC TCTTTGGTGC ACCCCCCCTTA GAGGAGGGGT ATGTGGTTCT GGTAGGAGAC 480  
AGAGGGCTAA AACGGTTTCC GCCCCCGTCT GAGTTTTTGC TTTCCGGTTG GAACCGAAGC 540  
CGCGCCGCGC GTCTTGTCTG CTGCAGCATC GTTCTGTGTT GTCTCTGTTT GACTGTTTTT 600  
CTGTATTTGT CTGAAAACAT GGGCCAGGCT GTTACCACCC CCTTAAGTTT GACTTTAGAC 660  
CACTGGAAGG ATGTCGAACG GACAGCCAC AACCTGTCCG TAGAGGTTAG AAAAAGGCGC 720  
TGGGTTACAT TCTGCTCTGC AGAATGGCCA ACCTTCAACG TCGGATGGCC ACGAGACGGC 780  
ACTTTTAACC CAGACATTAT TACACAGGTT AAGATCAAGG TCTTCTCACC TGGCCACAT 840  
GGACATCCGG ATCAGGTCCC CTACATCGTG ACCTGGGAAG CTATAGCAGT AGACCCCCCT 900  
CCCTGGGTCA GACCCCTCGT GCACCCTAAA CCTCCCCTCT CTCTTCCCCC TTCAGCCCCC 960  
TCTCTCCAC CTGAACCCCC ACTCTCGACC CCGCCCCAGT CCTCCCTCTA TCCGGCTCTC 1020  
ACTTCTCCTT TAAACACCAA ACCTAGGCCT CAAGTCCTTC CTGATAGCGG AGGACCACTC 1080  
ATTGATCTAC TCACGGAGGA CCCTCCGCCT TACCGGGACC CAGGGCCACC CTCTCCTGAC 1140  
GGGAACGGCG ATAGCGGAGA AGTGGCCCCCT ACAGAAGGAG CCCCTGACCC TTCCCCAATG 1200  
GTATCCCGCC TGCGGGGAAG AAAAGAACCC CCCGTGGCGG ATTCTACTAC CTCTCAGGCG 1260  
TTCCCCCTTC GCCTGGGAGG GAATGGACAG TATCAATACT GGCCATTTTC CTCCTCTGAC 1320  
CTCTATAACT GGAAAAATAA CAACCCCTCT TTCTCCGAGG ACCCAGCTAA ATTGACAGCT 1380  
TTGATCGAGT CCGTTCTCCT TACTCATCAG CCCACTTGGG ATGACTGCCA ACAGCTATTA 1440  
GGGACCCTGC TGACGGGAGA AGAAAAACAG CGAGTGCTCC TAGAGGCCCG AAAGGCGGTT 1500  
CGAGGGGAGG ACGGACGCCC AACTCAGCTG CCAATGACA TTAATGATGC TTTTCCCTTG 1560  
GAACGTCCCG ACTGGGACTA CAACACCAA CGAGGTAGGA ACCACCTAGT CCACTATCGC 1620  
CAGTTGCTCC TAGCGGGTCT CCAAAACGCG GGCAGAAGCC CCACCAATTT GGCCAAGGTA 1680  
AAAGGGATAA CCCAGGGACC TAATGAGTCT CCCTCAGCCT TTTTAGAGAG ACTCAAGGAG 1740  
GCCTATCGCA GATACACTCC TTATGACCCT GAGGACCCAG GGCAAGAAAC CAATGTGGCC 1800

FIGURE 5A

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ATGTCATTCA TCTGGCAGTC CGCCCCGGAT ATCGGGCGAA AGTTAGAGCG GTTAGAAGAT 1860  
TTGAAGAGTA AGACCTTAGG AGACTTAGTG AGGGAAGCTG AAAAGATCTT TAATAAACGA 1920  
GAAACCCCGG AAGAAAGAGA GGAACGTATT AGGAGAGAAA CAGAGGAAAA GGAAGAACGC 1980  
CGTAGGGCAG AGGATGTGCA GAGAGAGAAG GAGAGGGACC GCAGAAGACA TAGAGAAATG 2040  
AGTAAGTTGC TGGCTACTGT CGTTAGCGGG CAGAGACAGG ATAGACAGGG AGGAGAGCGA 2100  
AGGAGGCCCC AACTCGACCA CGACCAGTGT GCCTACTGCA AAGAAAAGGG ACATTGGGCT 2160  
AGAGATTGCC CCAAGAAGCC AAGAGGACCC CGGGGACCAC GACCCAGGC CTCCCTCCTG 2220  
ACCTTAGACG ATTAGGGAAG TCAGGGTCAG GAGCCCCCCC CTGAACCCAG GATAACCCTC 2280  
AGAGTCGGGG GGCAACCCGT CACCTTCCTA GTGGATACTG GGGCCCAACA CTCCTGCTG 2340  
ACCCAAAATC CTGGACCCCT AAGTGACAAG TCTGCCTGGG TCCAAGGGGC TACTGGAGGG 2400  
AAGCGGTATC GCTGGACCAC GGATCGCCGA GTGCACCTAG CCACCGGTAA GGTCACCCAT 2460  
TCTTTCCTCC ATGTACCAGA TTGCCCCTAT CCTCTGCTAG GAAGAGATT TCTGACTAAA 2520  
CTAAAAGCCC AAATTCACCT TGAGGGATCA GGAGCTCAGG TTGTGGGACC AATGGGACAG 2580  
CCCCTGCAAG TGCTGACCCT AAACATAGAA GATGAGTATC GGCTACATGA GACCTCAAAA 2640  
GGGCCAGATG TGCCTCTAGG GTCCACATGG CTCTCTGATT TTCCCCAGGC CTGGGCAGAA 2700  
ACCGGGGGCA TGGGGCTGGC CGTTCGCCAA GCTCCTCTGA TCATACCTCT GAAGGCAACC 2760  
TCTACCCCCG TGTCCATAAA ACAATACCCC ATGTCACAAG AAGCCAGACT GGGGATCAAG 2820  
CCCCACATAC AGAGACTGCT GGATCAGGGA ATTCTGGTAC CTTGCCAGTC CCCCTGGAAC 2880  
ACGCCCCCTGC TACCCGTTAA GAAACCGGGG ACTAATGATT ATAGGCCTGT CCAGGATCTG 2940  
AGAGAAGTCA ACAAGCGGGT GGAAGACATC CACCCACCG TGCCCAACCC TTACAACCTC 3000  
TTGAGCGGGC TCCCACCGTC CCACCAGTGG TACACTGTGC TTGACTTAAA AGATGCTTTT 3060  
TTCTGCCTGA GACTCCACCC CACCAGTCAG TCTCTCTCG CTTTGAGTG GAGAGATCCA 3120  
GAGATGGGAA TCTCAGGACA ATTAACCTGG ACCAGACTCC CGCAGGGTTT CAAAAACAGT 3180  
CCCACCCTGT TTGATGAAGC CCTGCACAGG GACCTCGCAG ACTTCCGGAT CCAGCACCCA 3240  
GACCTGATTC TGCTCCAGTA TGTAAGTAC TTAAGTCTGG CCGCCACTTC TGAGCTTGAC 3300  
TGTCACAAG GTACGCGGGC CCTGTTACAA ACCCTAGGGG ACCTCGGATA TCGGGCCTCG 3360  
GCCAAGAAAG CCCAAATTTG CCAGAAACAG GTCAAGTATC TGGGGTATCT TCTAAAAGAG 3420  
GGTCAGAGAT GGCTGACTGA GGCCAGAAAA GAGACTGTGA TGGGGCAGCC TACTCCGAAG 3480  
ACCCCTCGAC AACTAAGGGA GTTCCTAGGG ACGGCAGGCT TCTGTGCGCT CTGGATCCCT 3540  
GGGTTTGACG AAATGGCAGC CCCCTTGATC CCTCTACCA AAACGGGGAC TCTGTTTGAC 3600  
TGGGGCCCAG ACCAGCAAAA GGCCTACCAA GAGATCAAGC AGGCTCTCTT AACTGCCCCCT 3660

FIGURE 5B

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GCCCTGGGAT TGCCAGACTT GACTAAGCCC TTCGAACTTT TTGTTGACGA GAAGCAGGGC 3720  
TACGCCAAAG GTGTCCTAAC GCAAAAAGT GGGCCTTGCC GTCGGCCGGT GGCCTACCTG 3780  
TCCAAAAGC TAGACCCAGT GGCAGCTGGG TGGCCCCCTT GCCTACGGAT GGTAGCAGCC 3840  
ATCGCCGTTT TGACCAAAGA CGCTGGCAAG CTCACCATGG GACAGCCACT AGTCATTCTG 3900  
GCCCCCATG CAGTAGAGGC ACTAGTTAAG CAACCCCTG ATCGCTGGCT CTCCAACGCC 3960  
CGAATGACCC ACTACCAGGC TCTGCTTCTG GACACGGACC GAGTCCAGTT CGGACCAATA 4020  
GTGGCCCTAA ACCCAGCTAC GCTGCTCCCT CTACCTGAGG AGGGGCTGCA ACATGACTGC 4080  
CTTGACATCT TGGCTGAAGC CCACGGAAGT AGACCAGATC TTACGGACCA GCCTCTCCCA 4140  
GACGCTGACC ACACCTGGTA CACAGATGGG AGCAGCTTCC TGCAAGAGGG GCAGCGCAAG 4200  
GCCGGAGCAG CAGTAACCAC CGAGACCGAG GTAGTCTGGG CCAAAGCACT GCCAGCCGGG 4260  
ACATCGGCCC AAAGAGCTGA GTTGATAGCG CTCACCCAAG CCTTAAAAAT GGCAGAAGGT 4320  
AAGAAGCTGA ATGTTTACAC CGATAGCCGT TATGCTTTTG CCACTGCCCA TATTCACGGA 4380  
GAAATATATA GAAGGCGCGG GTTGCTCACA TCAGAAGGAA AAGAAATCAA AAATAAGGAC 4440  
GAGATCTTGG CCCTACTGAA GGCTCTCTTC CTGCCCAAAA GACTTAGCAT AATTCATTGC 4500  
CCGGGACATC AGAAGGGGAA CCGCGCGGAG GCAAGGGGCA ACAGGATGGC CGACCAAGCG 4560  
GCCCCGAGAAG TAGCCACTAG AGAACTCCA GAGACTTCCA CACTTCTGAT AGAAAATTCA 4620  
GCCCCCTATA CTCATGAACA TTTTCACTAT ACGGTGACTG ACATAAAAGA TCTGACTAAA 4680  
CTAGGGGCCA CTTATGACGA TGCAAAGAAG TGTGGGTTT ATCAGGGAAA GCCTGTAATG 4740  
CCTGATCAAT TCACCTTGA ACTATTAGAT TTTCTTCATC AATTGACCCA CCTCAGTTTC 4800  
TCAAAAACAA AGGCTCTTCT AGAAAGGAAC TACTGTCTT ATTACATGCT GAACCGGGAT 4860  
CGAACGCTCA AAGACATCAC TGAGACTTGC CAAGCCTGTG CACAGGTCAA TGCCAGCAAG 4920  
TCTGCCGTCA AACAAGGGAC TAGAGTTCGA GGGCACCGAC CCGGCACCCA CTGGGAAATT 4980  
GATTTCACTG AGGTAAAACC TGGCCTGTAT GGGTATAAAT ATCTTTTAGT TTTCATAGAC 5040  
ACTTTCTCTG GATGGGTAGA AGCTTTCCCA ACCAAGAAAG AAAGTGCCAA AGTTGTAACC 5100  
AAGAAGCTAC TAGAAGAAAT CTTCCCCAGA TTCGGCATGC CACAGGTATT GGGAACCGAC 5160  
AATGGGCCTG CCTTCGTCTC CAAGGTAAAGT CAGACAGTAG CCGATTACT GGGGGTTGAT 5220  
TGGAAGCTAC ATTGTGCTTA CAGACCCAG AGTTCAGGTC AGGTAGAAAG AATGAATAGG 5280  
ACAATCAAGG AGACTTTAAC TAAATTGACG CTTGCAACTG GCTCTAGGGA CTGGGTGCTC 5340  
CTGCTTCCCC TAGCCCTGTA TCGAGCCCGC AACACGCCGG GCCCCCATGG TCTCACCCCA 5400

FIGURE 5C

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TATGAAATCT TATATGGGGC ACCCCCGCCC CTTGTAAACT TCCCTGATCC TGACATGGCA 5460  
 AAGGTTACTC ATAACCCCTC TCTCCAAGCC CATTTACAGG CACTCTACCT GGTCCAGCAC 5520  
 GAAGTCTGGA GACCGTTGGC GGCAGCTTAC CAAGAACAAC TGGACCGGCC GGTAGTGCCT 5580  
 CACCCTTTCC GAGTCGGTGA CACAGTGTGG GTCCGCAGAC ACCAAACTAA AAATCTAGAA 5640  
 CCCCCTGGA AAGGACCTTA TACCGTCCTA CTGACTACCC CCACCGCTCT CAAAGTGGAC 5700  
 GGCATTGCAG CGTGGATCCA CGCTGCCAC GTAAAGGCTG CCGACACCAG GATTGAGCCA 5760  
 CCATCGGAAT CGACATGGCG TGTTC AACGC TCTCAAAATC CCCTAAAGAT AAGATTGACC 5820  
 >REFMLVCGD. ENV  
 CGCGGGACCT CCTAATCCCC TTAATCTCT TCCTGTCTCT CAAAGGGGCC AGATCCGCAG 5880  
 REFMLVCGD. POL<  
 CACCCGGCTC CAGCCCTCAC CAGGTCTACA ACATTACCTG GGAAGTGACC AATGGGGATC 5940  
 GGGAGACAGT ATGGGCAATA TCAGGCAACC ACCCTCTGTG GACTTGGTGG CCAGTCCTCA 6000  
 CCCAGATTT GTGTATGTTA GCTCTCAGTG GGCCGCCCCA CTGGGGGCTA GAGTATCAGG 6060  
 CCCCCTATTC CTCGCCCCCG GGGCCCCCTT GTTGCTCAGG GAGCAGCGGG AACGTTGCAG 6120  
 GCTGTGCCAG AGACTGCAAC GAGCCCTTGA CCTCCCTCAC CCCTCGGTGC AACACTGCCT 6180  
 GGAACAGACT TAAGCTGGAC CAGGTAATC ATAAATCAAG TGAGGGATTT TATGTCTGCC 6240  
 CCGGGTCACA TCGCCCCCGG GAAGCCAAGT CCTGTGGGGG TCCAGACTCC TTCTACTGTG 6300  
 CCTCTTGGGG CTGCGAGACA ACCGGTAGAG TATACTGGAA GCCCTCCTCT TCTTGGGACT 6360  
 ACATCACAGT AGACAACAAT CTCACCTCTA ACCAGGCTGT TCAGGTATGC AAAGACAATA 6420  
 AGTGGTGCAA TCCCTTGGCT ATCCGGTTTA CAAACGCCGG GAAACAGGTC ACCTCATGGA 6480  
 CAACTGGACA CTATTGGGGT CTACGTCTTT ATGTCTCTGG ACAGGACCCA GGGCTTACTT 6540  
 TCGGGATCCG ACTCAGTTAT CAAAATCTAG GACCTCGGAT CCAATAGGA CCAAACCCCG 6600  
 TCCTGGCAGA CCAACTTTCG TTCCCGCTAC CTAATCCCCT ACCCAAACCT GCCAAGTCTC 6660  
 CCCCCGCCTC TAGTTCGACT CCCACATTGA TTTCCCCGTC CCCCCTCCC ACTCAGCCCC 6720  
 CGCCAGCAGG AACGGGAGAC AGATTACTAA ATCTAGTACA GGGAGCTTAC CAGGCACTCA 6780  
 ACCTTACCAA CCCTGATAAA ACTCAAGAGT GCTGGTTATG CCTAGTGTCT GGACCCCCCT 6840  
 ATTACGAGGG GGTGCGGTC CTAGGTACTT ATTCCAACCA TACCTCTGCC CCAGCTAACT 6900  
 GCTCCGTGGC CTCCCAACAC AAGCTGACCC TGTCCGAAGT GACTGGACGG GGA CTCTGCA 6960  
 TAGGAACAGT CCAAAAACT CACCAGGCCC TGTGCAACAC TACCCTTAAG GCAGGCAAAG 7020  
 GGTCTTACTA TCTAGTTGCC CCCACAGGAA CTATGTGGGC ATGTAACACT GGA CTCACTC 7080  
 CATGCCTATC TGCCACCGTG CTTAATCGCA CCACTGACTA TTGCGTTCTC GTGGAATTAT 7140

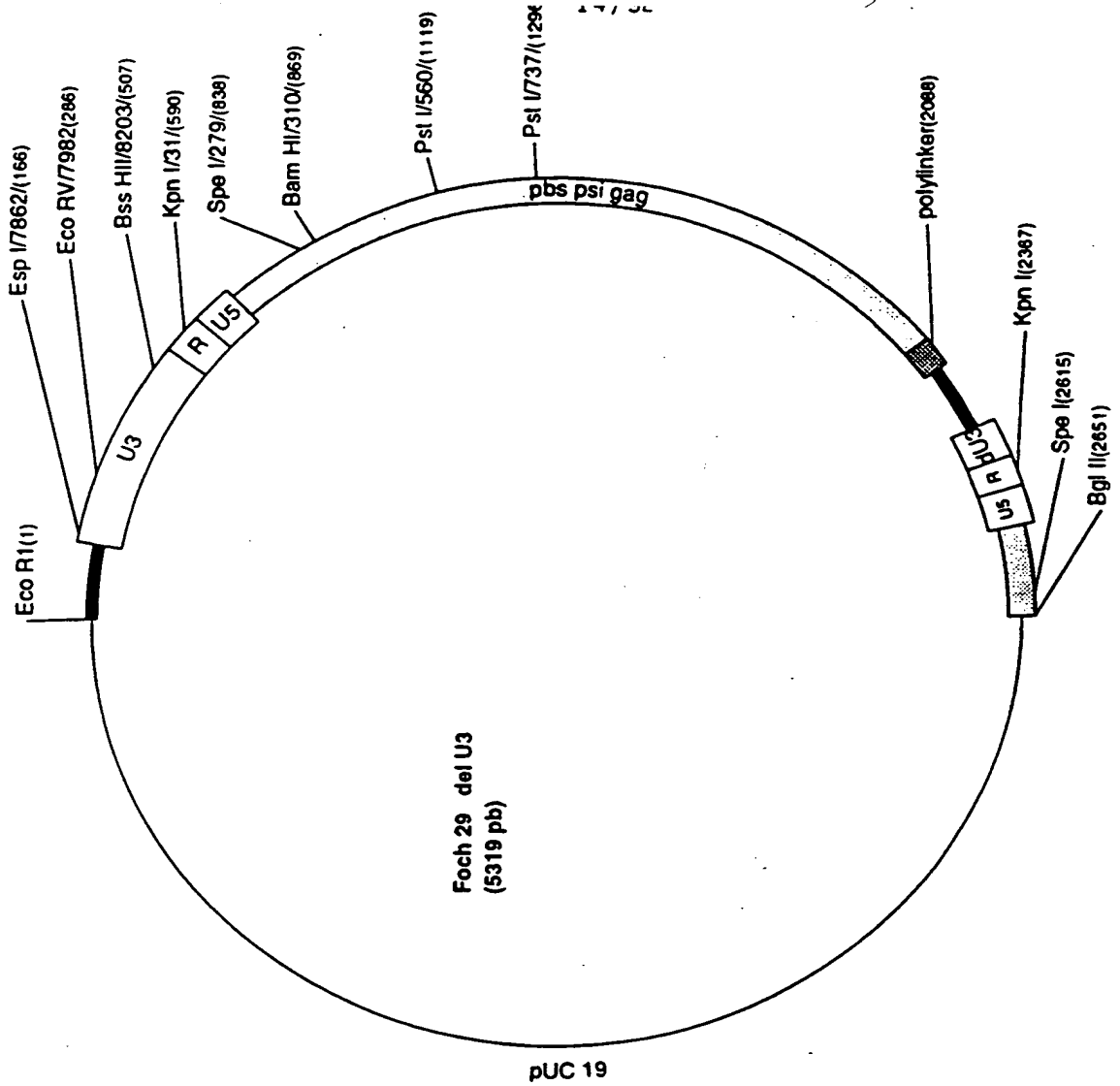
FIGURE 5D

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GGCCCAGGGT CACCTACCAT CCTCCCAGTT ACGTCTATAG CCAGTTTGAA AAATCCCATA 7200  
GACATAAAAG AGAACCAGTG TCCTTAACCT TGGCCTTATT ATTAGGTGGG CTAACCTATGG 7260  
GTGGCATCGC CGCGGGAGTA GGGACAGGAA CTACCGCCCT GGTGCGCCACC CAGCAGTTTC 7320  
AGCAGCTCCA TGCTGCCGTA CAAGATGATC TCAAAGAAGT CGAAAAGTCA ATTACTAACC 7380  
TAGAAAAGTC TCTTACTTCG TTGTCTGAGG TTGTACTGCA GAATCGACGA GGCCTAGACC 7440  
TGTTGTTTCT AAAAGAGGGA GGACTGTGTG CTGCCCTAAA AGAAGAATGT TGTTCCTATG 7500  
CTGACCATAC AGGCCTAGTA AGAGATAGTA TGGCCAAATT AAGAGAGAGA CTCTCTCAGA 7560  
GACAAAAACT ATTTGAGTCG AGCCAAGGAT GGTTCGAAGG ATGGTTTAAC AGATCCCCCT 7620  
GGTTTACCAC GTTGATATCC ACCATCATGG GGCCTCTCAT TATACTCCTA CTAATTCCTG 7680  
TTTTTGACC CTGCATTCTT AATCGATTAG TTCAATTGT TAAAGACAGG ATCTCAGTAG 7740  
TCCAGGCTTT AGTCCTGACT CAACAATACC ACCAGCTAAA ACCACTAGAA TACGAGCCAC 7800  
AATAAATAAA AGATTTTATT TAGTTTCCAG AAAAAGGGGG GAATGAAAGA CCCCACCAA 7860  
TTGCTTAGCC TGATAGCCGC AGTAACGCCA TTTTGCAAGG CATGGAAAAA TACCAAACCA 7920  
AGAATAGAGA AGTTCAGATC <sup>LTR 81</sup> AAGGGCGGGT ACACGAAAAC AGCTAACGTT GGGCCAAACA 7980  
GGATATCTGC GGTGAGCAGT TTCGGCCCCG GCGCGGGGCC AAGAACAGAT GGTCACCGCG 8040  
GTTGCGCCCC GCGCGGGGCC CAAGAACAGA TGGTCCCCAG ATATGGCCCA ACCCTCAGCA <sup>LTR + 282</sup> 8100  
GTTTCTTAAG ACCCATCAGA TGTTTCCAGG CTCCCCCAAG <sup>U3</sup> GACCTGAAAT <sup>R</sup> GACCCTGTGC 8160  
CTTATTTGAA TTAACCAATC AGCCTGCTTC TCGCTTCTGT TCGCGCGCTT CTGCTTCCCG 8220  
AGCTCTATAA AAGAGCTCAC AACCCTCAC TCGGCGCGCC AGTCCTCCGA TAGACTGAGT 8280  
CGCCCGGGTA CCCGTGTATC CAATAAATCC TCTTGCTGTT GCA 8323

FIGURE 5E

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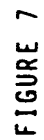
polylinker :  
Bam HI : 2088  
Xba I : 2094  
Sal I : 2100  
Pst I : 2106  
Sph I : 2112

FIGURE 6

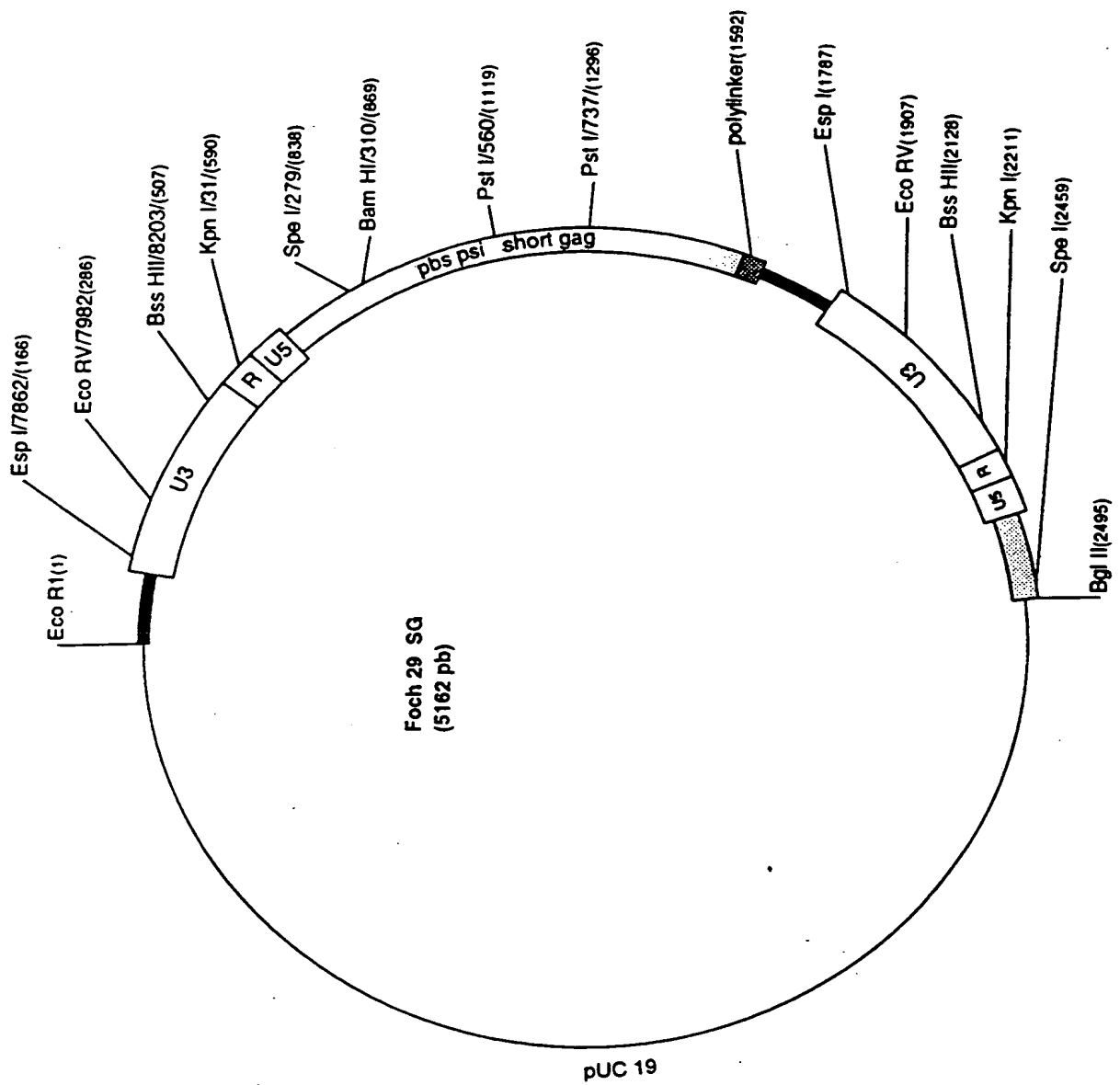
FIGURE 6

5' AAT TCA ATG AAA GAC CCC ACC AAA TTG C 3'  
3' GT TAC TTT CTG GGG TGG TTT AAC GAA T 5'

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polylinker :  
Bam HI : 1592  
Xba I : 1598  
Sal I : 1604  
Pst I : 1610  
Sph I : 1616

FIGURE 8

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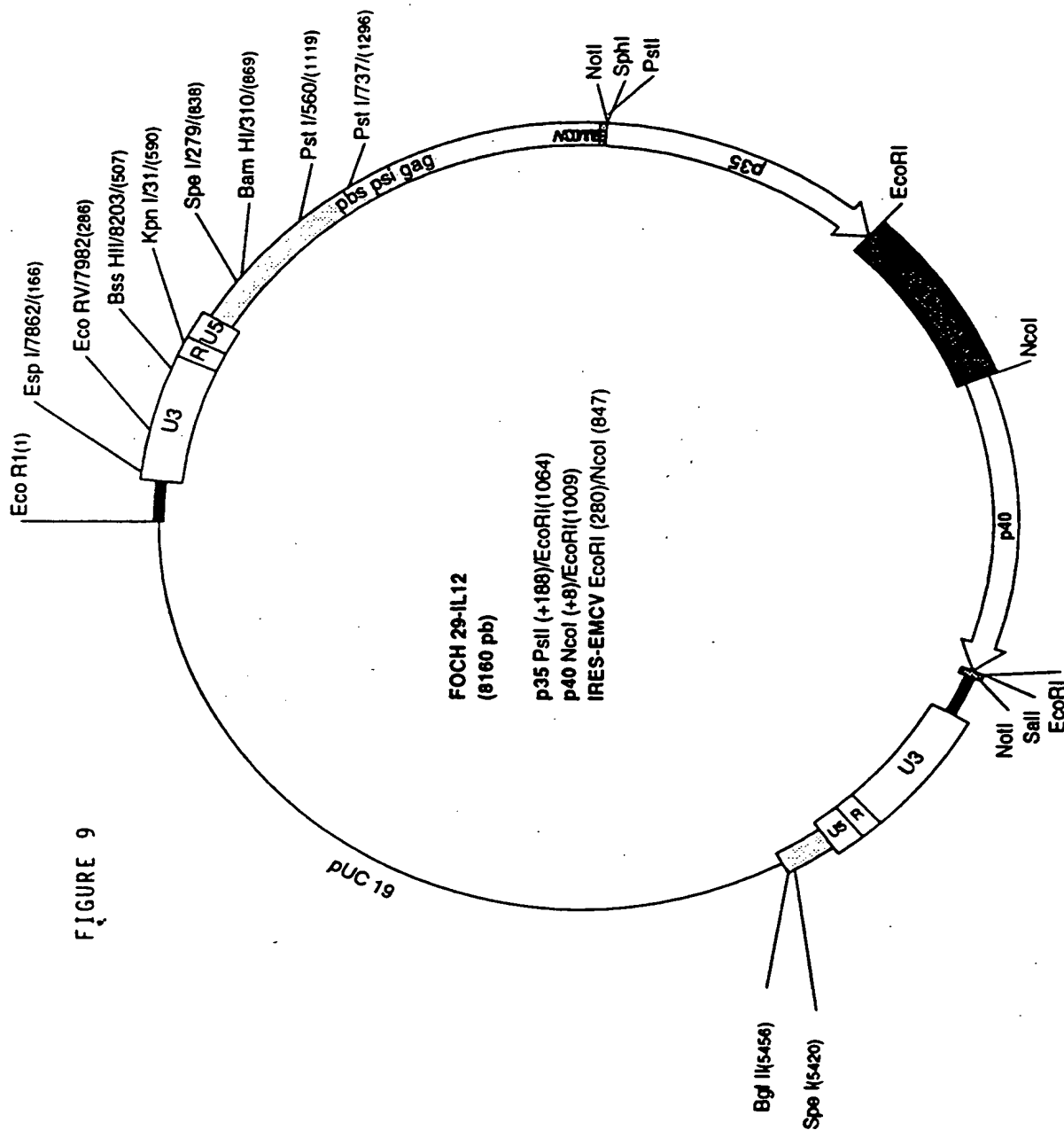


FIGURE 9

FOCH 29-IL12 (8160 pb)

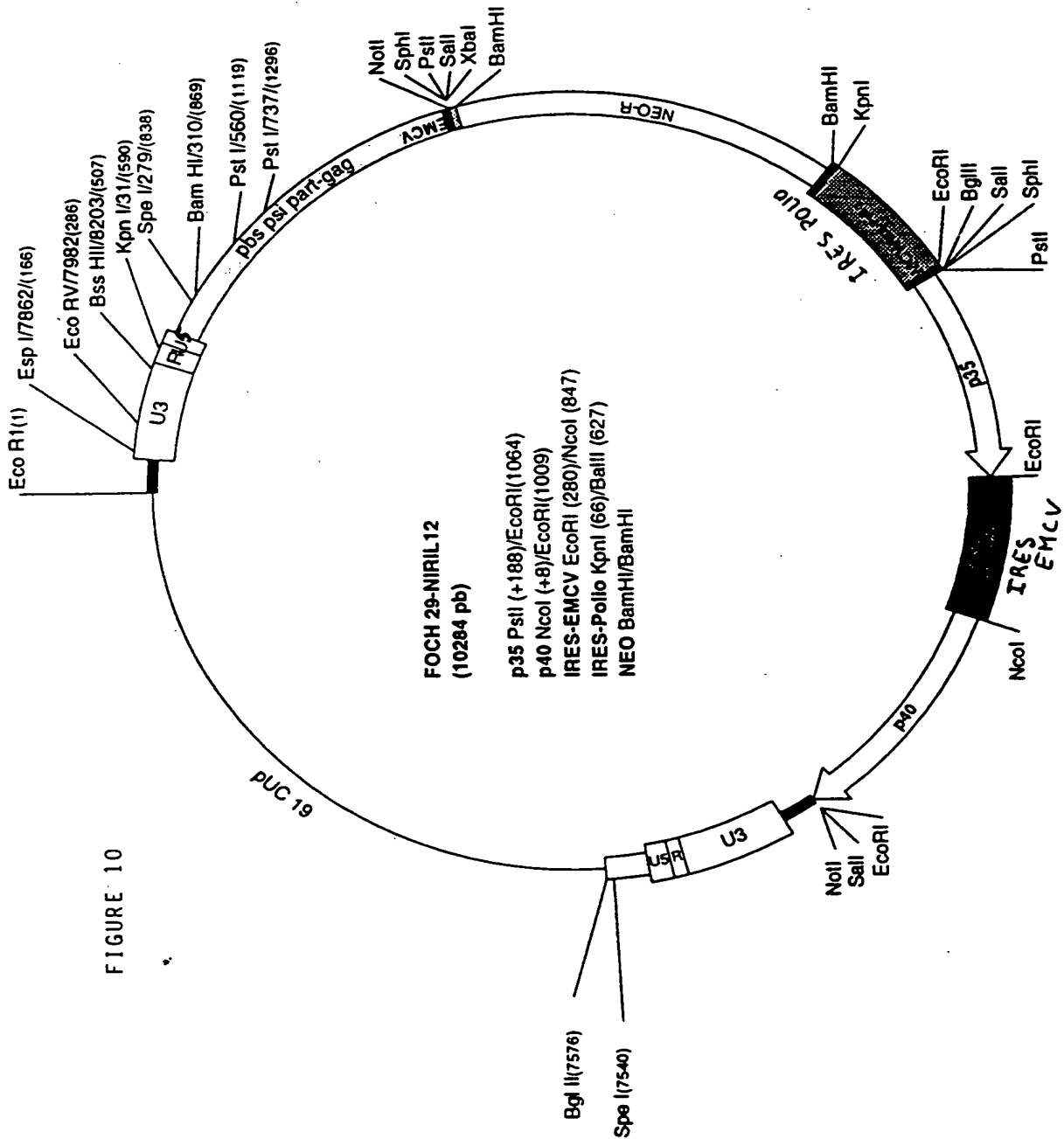


FIGURE 10

FOCH 29-NIRIL12

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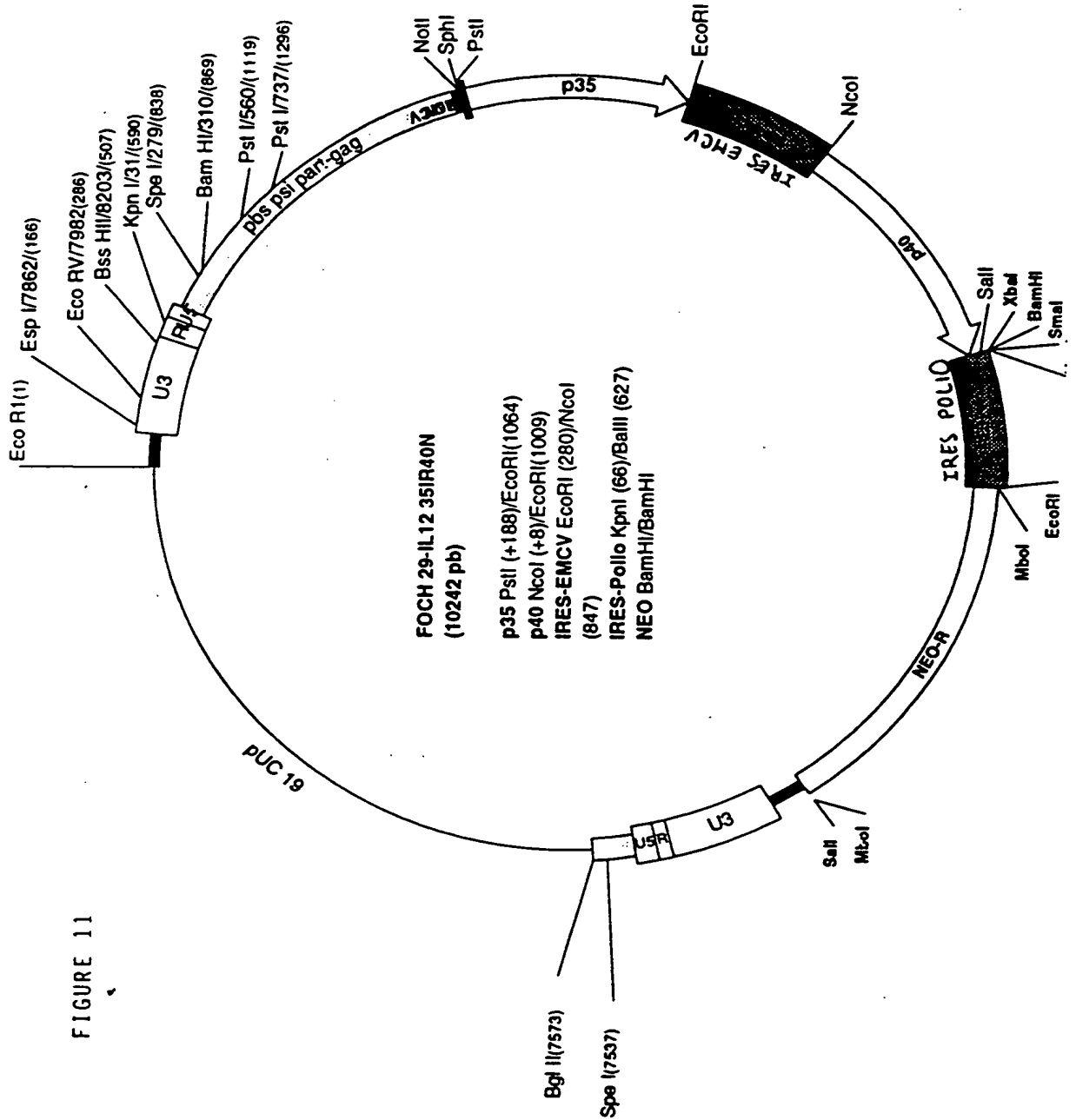
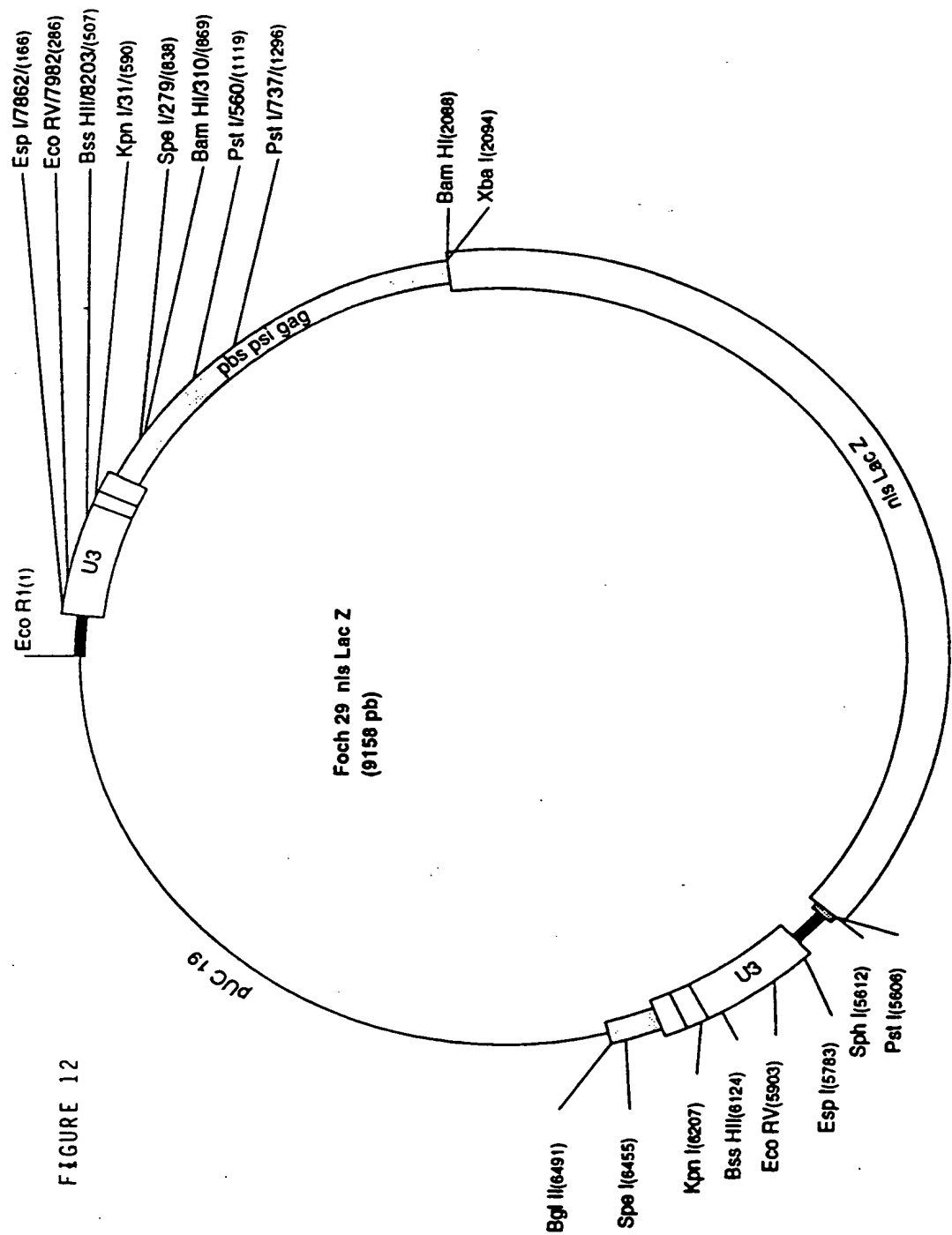


FIGURE 11

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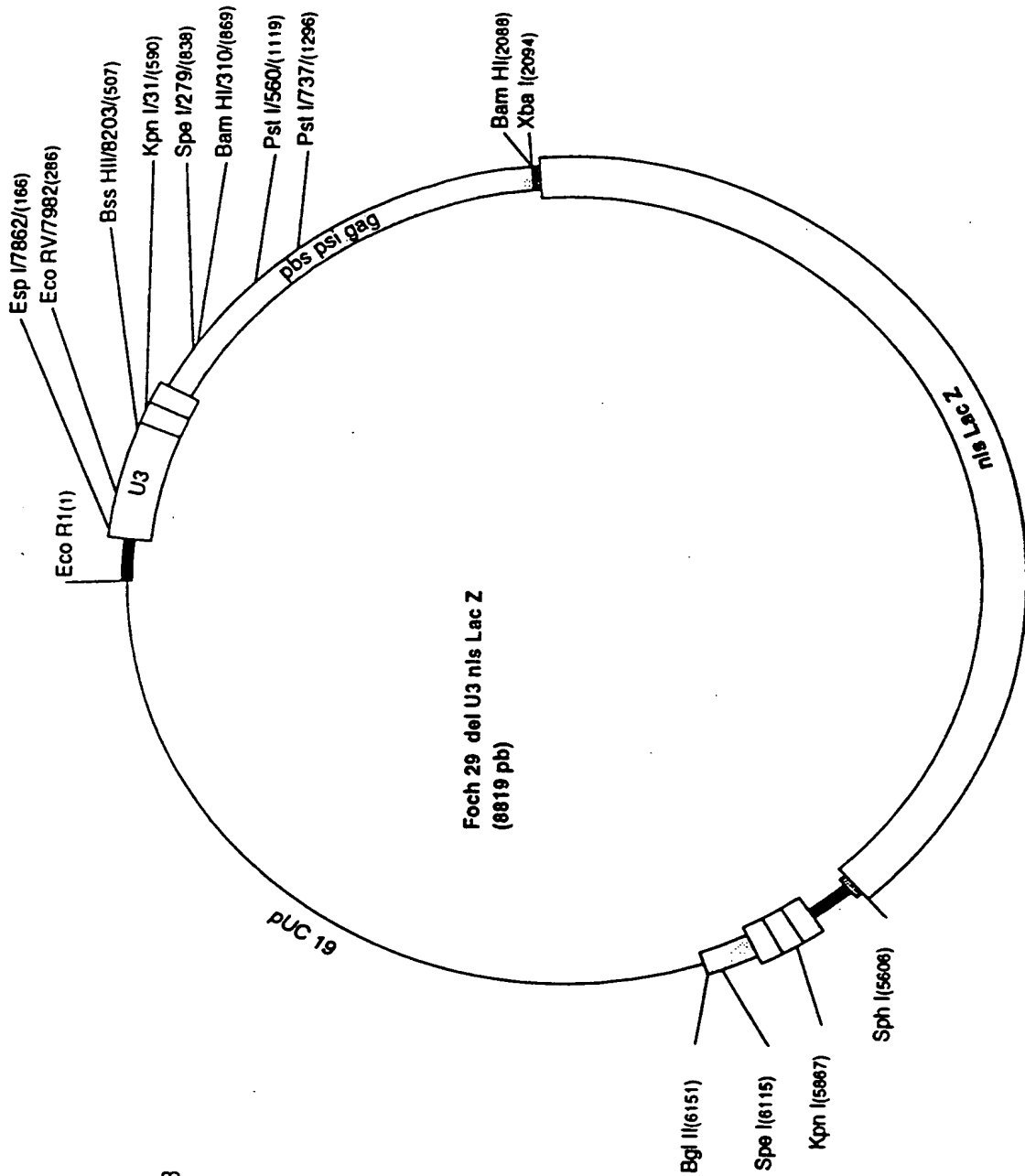


FIGURE 13

FIGURE 13

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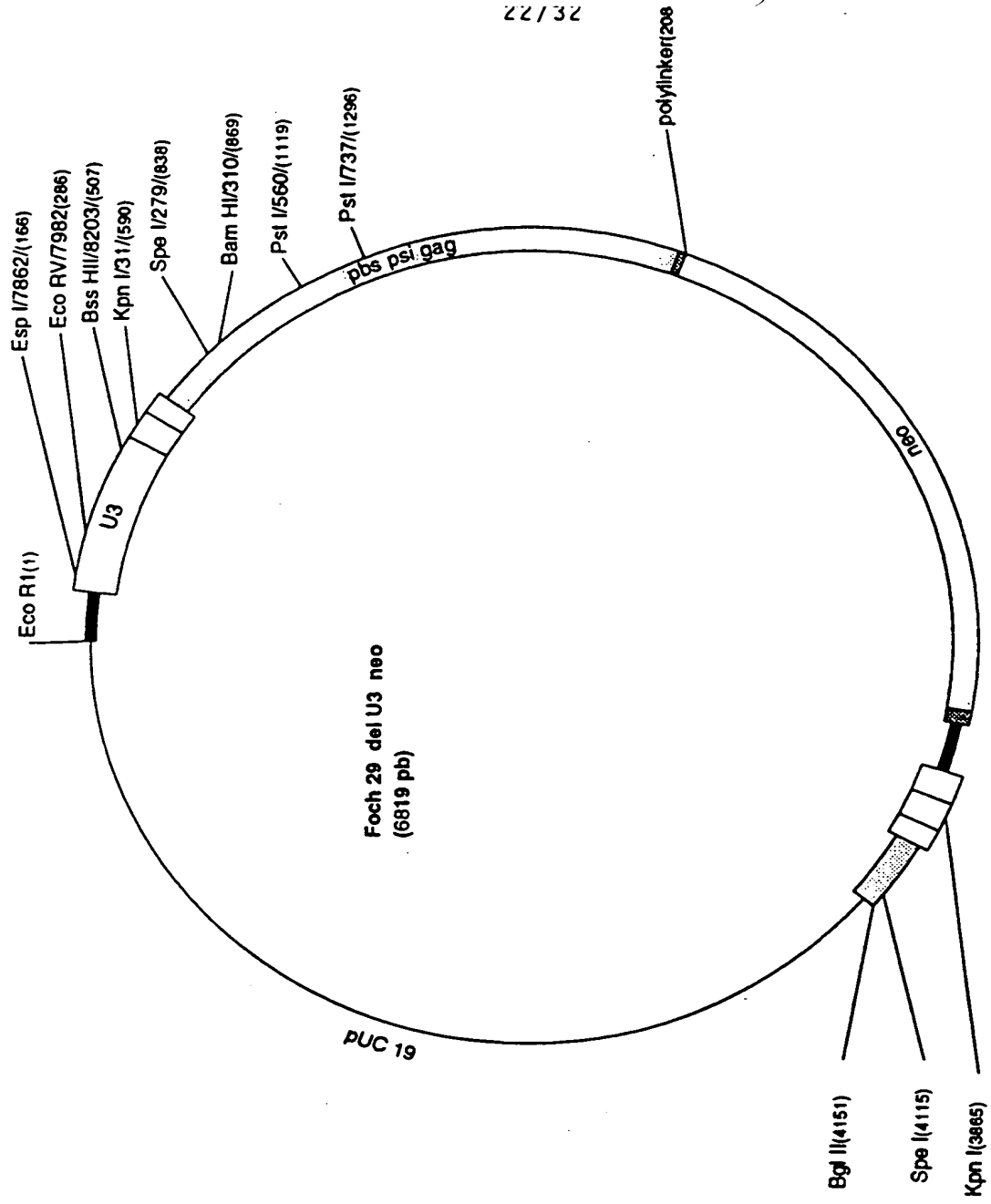


FIGURE 14

FIGURE 14

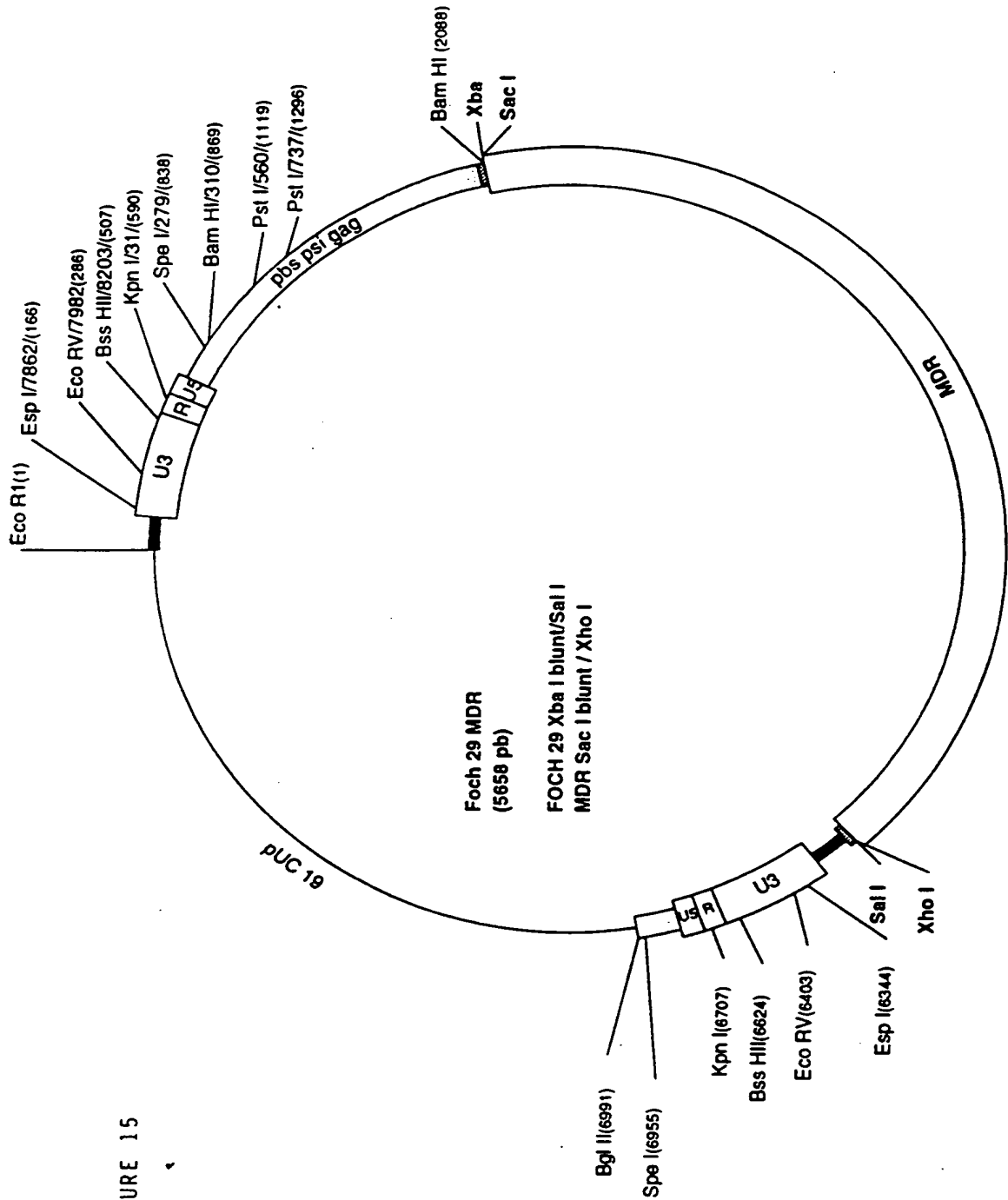
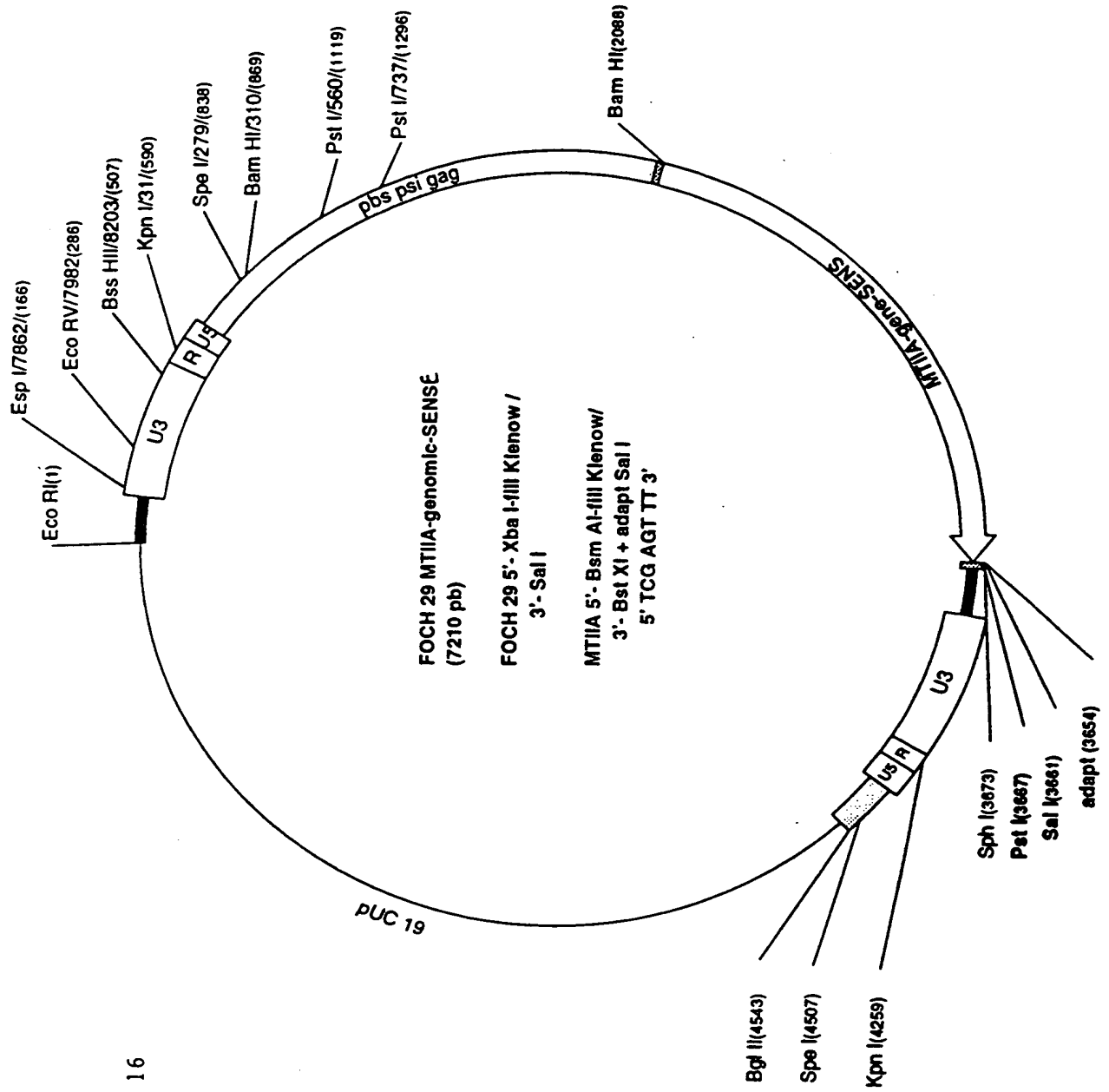


FIGURE 15

FOCH 29 MDR (5658 pb)

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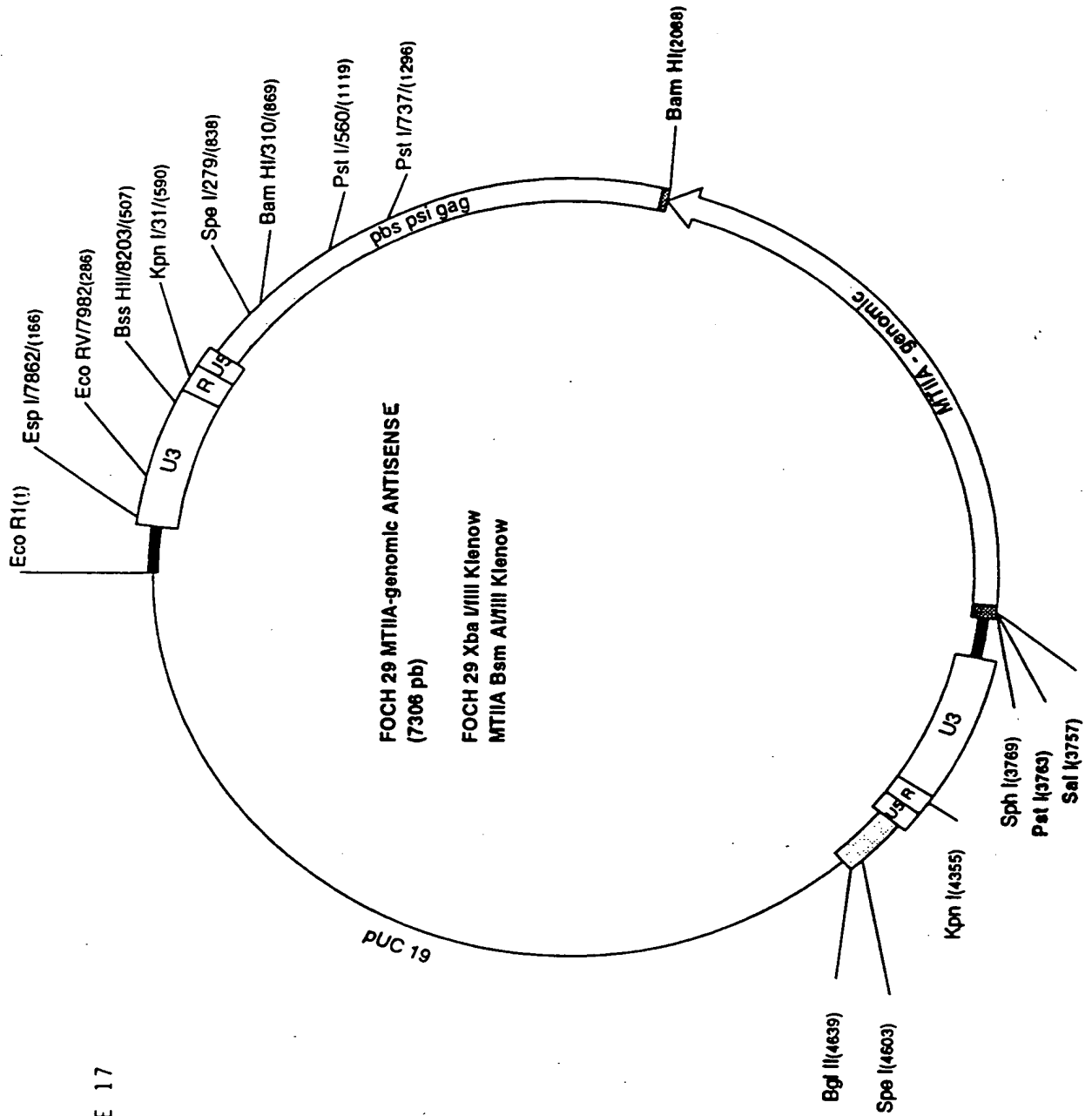
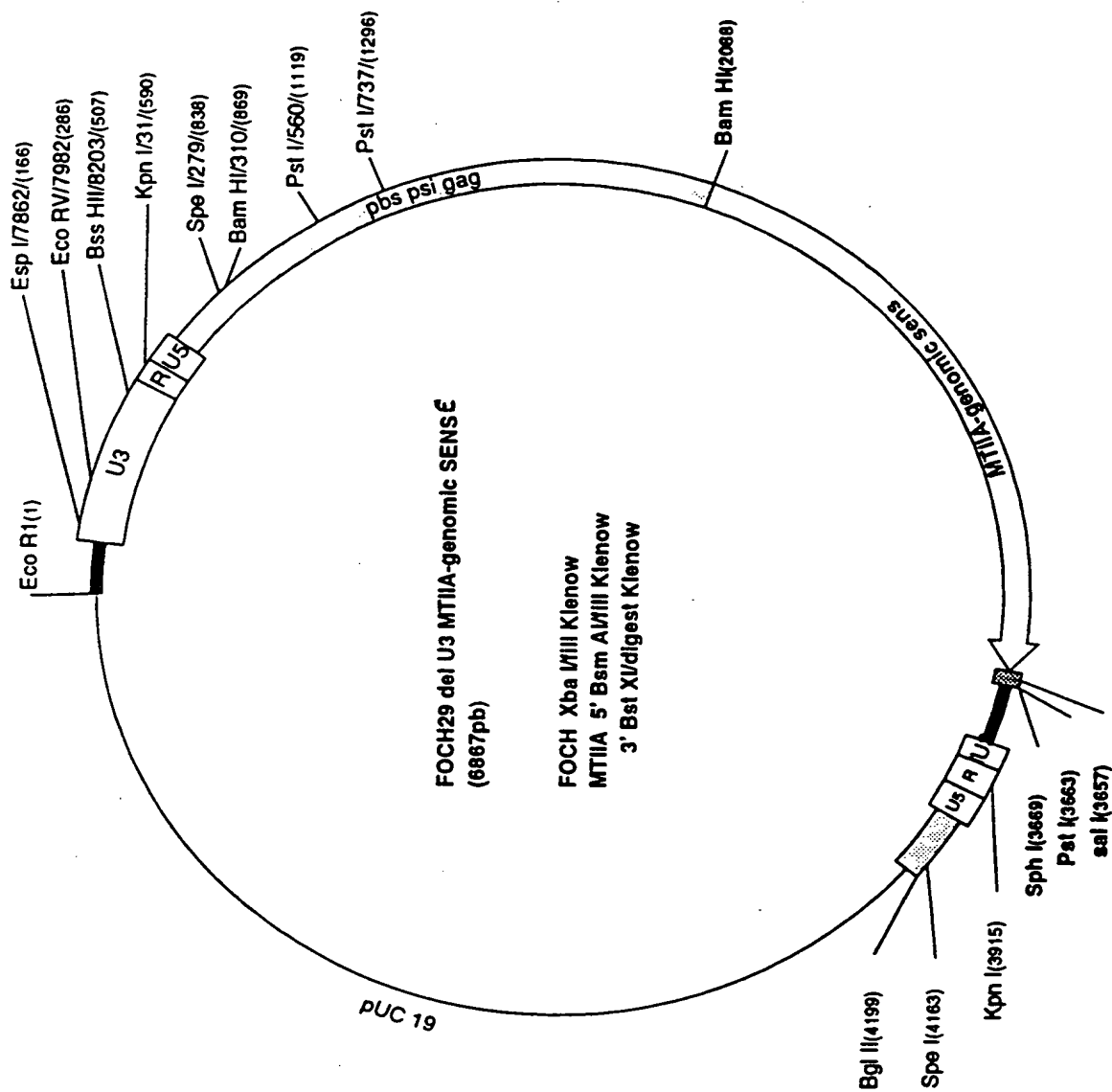


FIGURE 17

104007-26502650

FIGURE 18



FOOT 26504650

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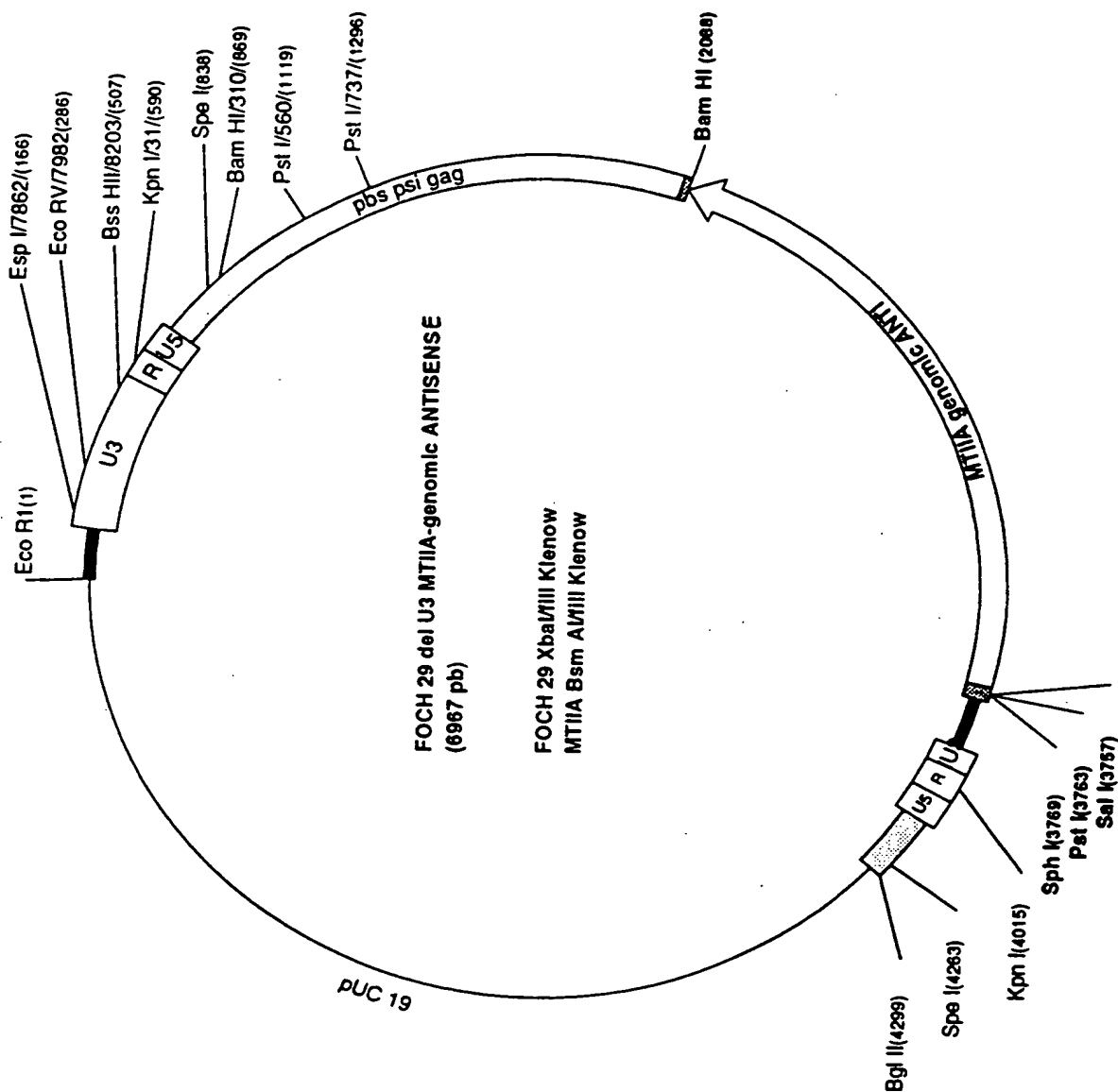


FIGURE 19

[illegible]

Inventor: COHEN-HAGUENAUER  
Docket No.: 8076.110USC2  
Title: RETROVIRAL VECTOR FOR THE TRANSFER AND EXPRESSION OF GENES FOR  
THERAPEUTIC PURPOSES IN EUKARYOTIC CELLS  
Attorney Name: Katherine M. Kowalchyk  
Phone No.: 612-371-5311  
Sheet 28 of 32

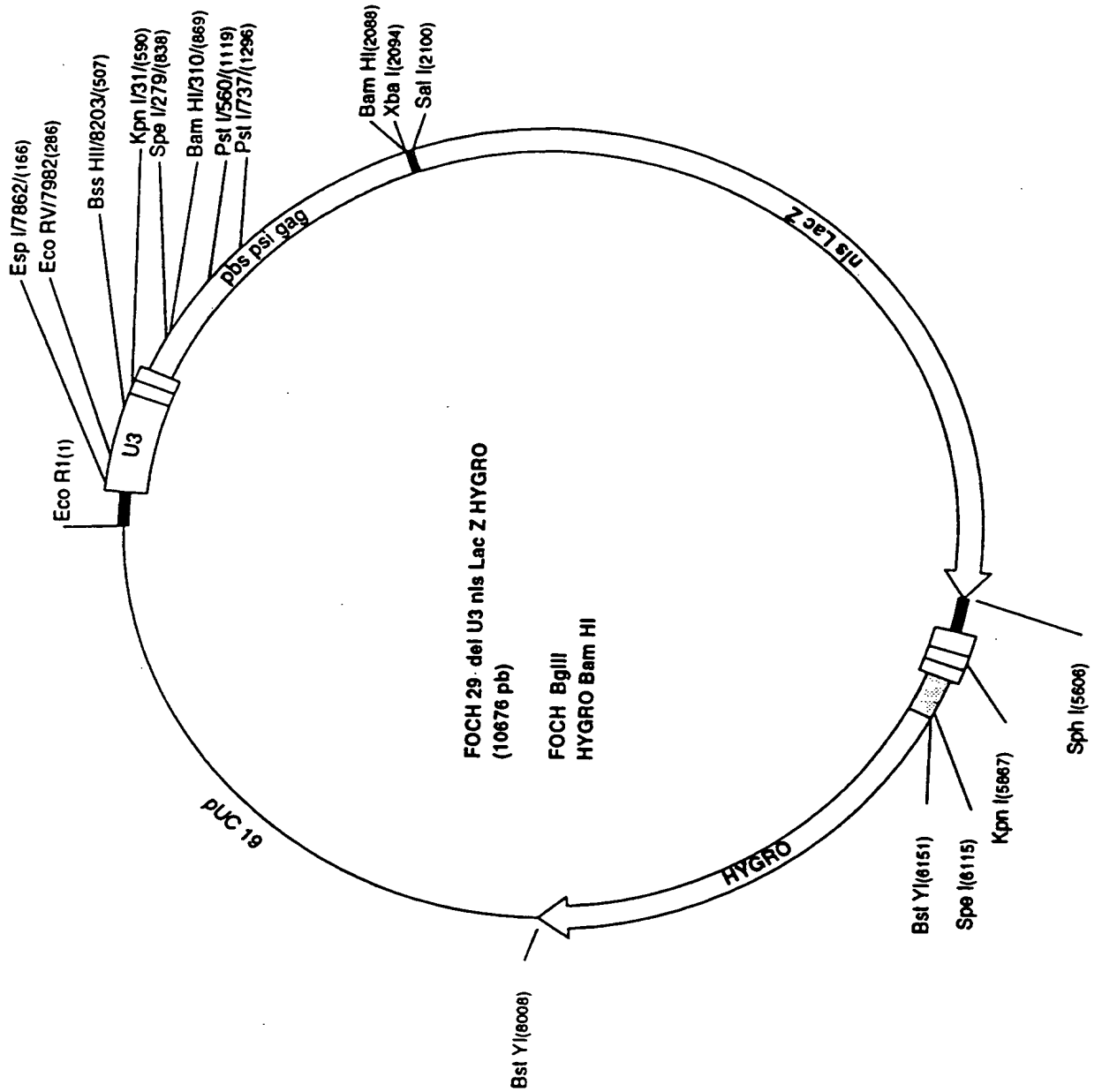


FIGURE 21

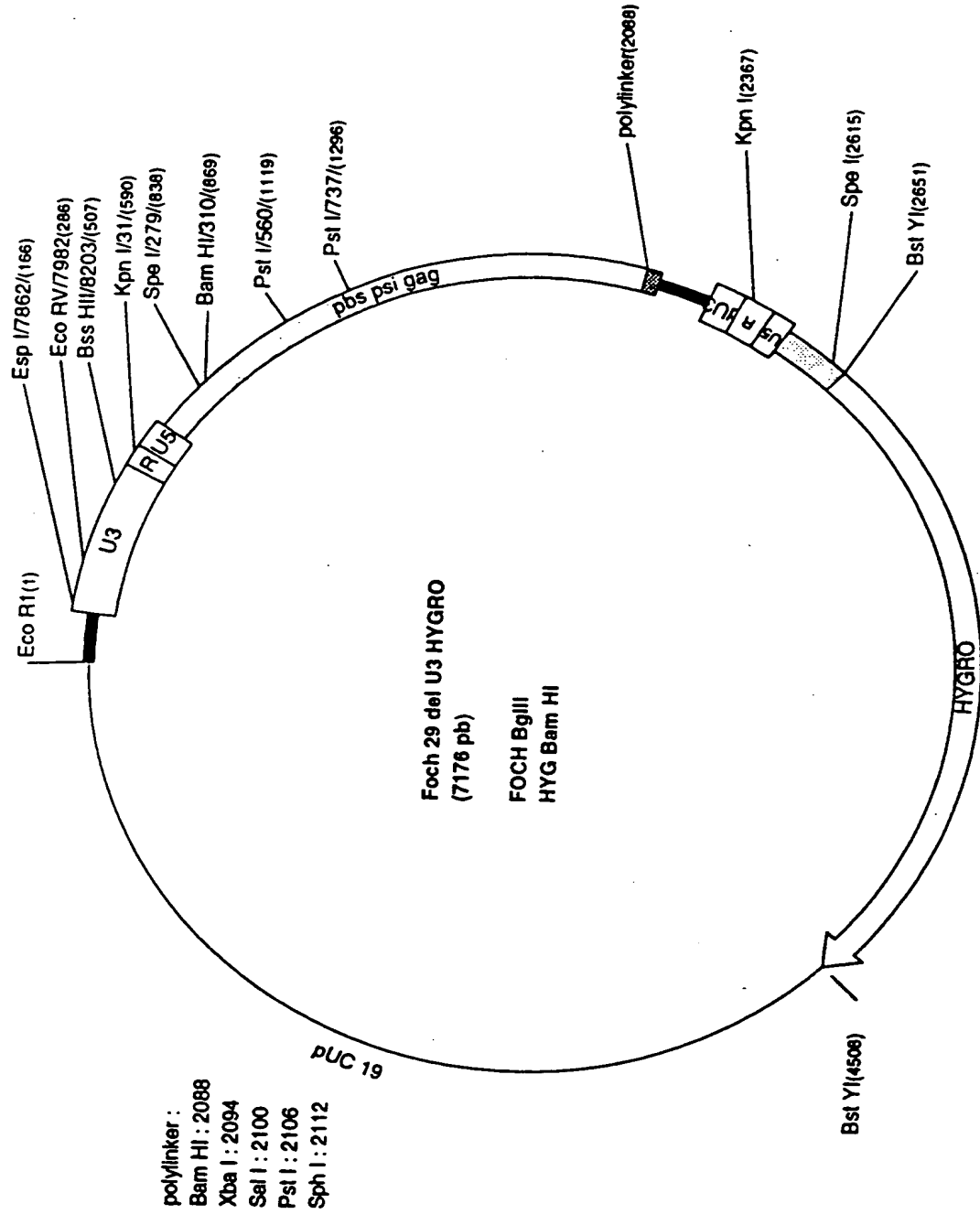
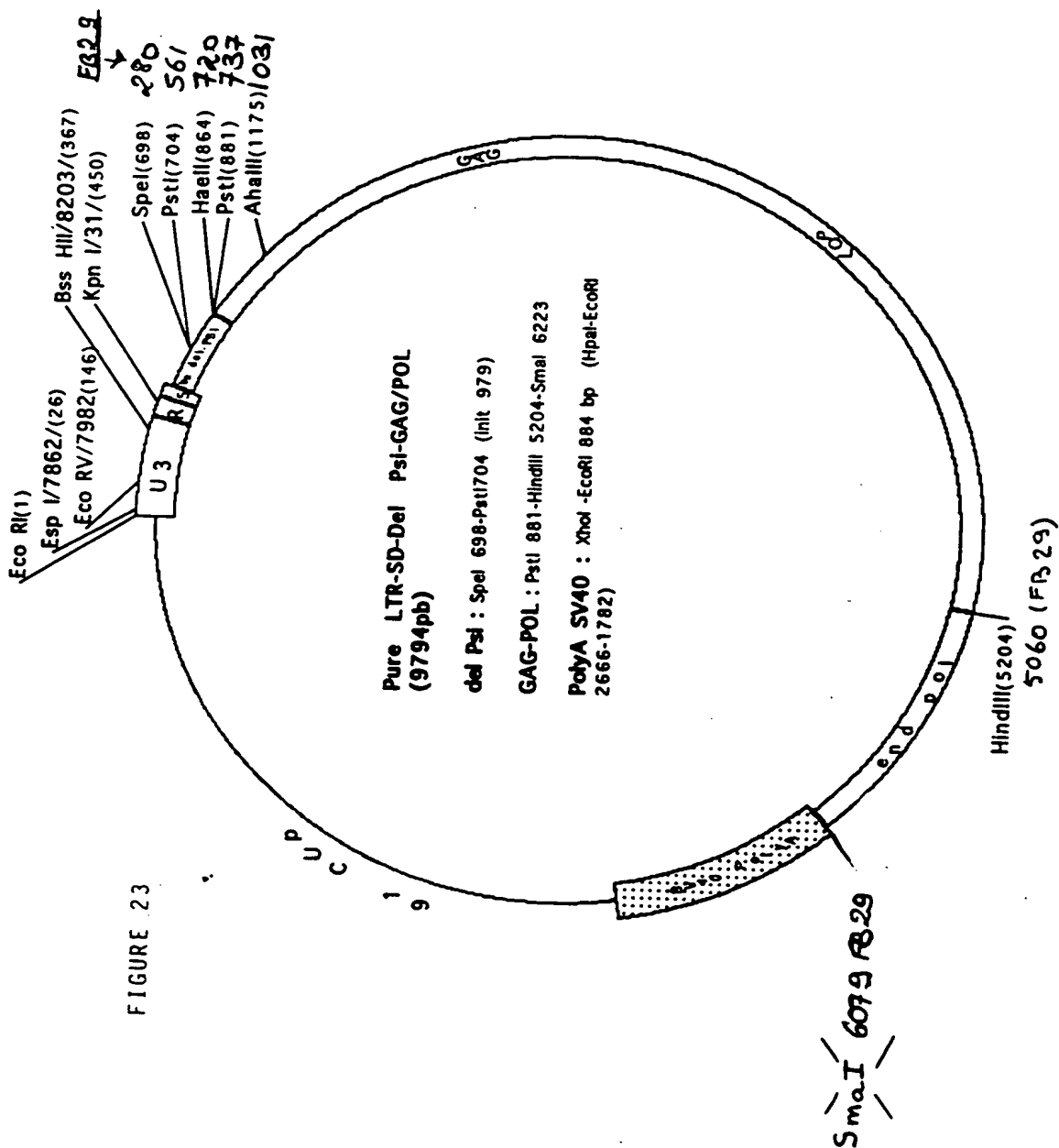


FIGURE 22

FIGURE 23



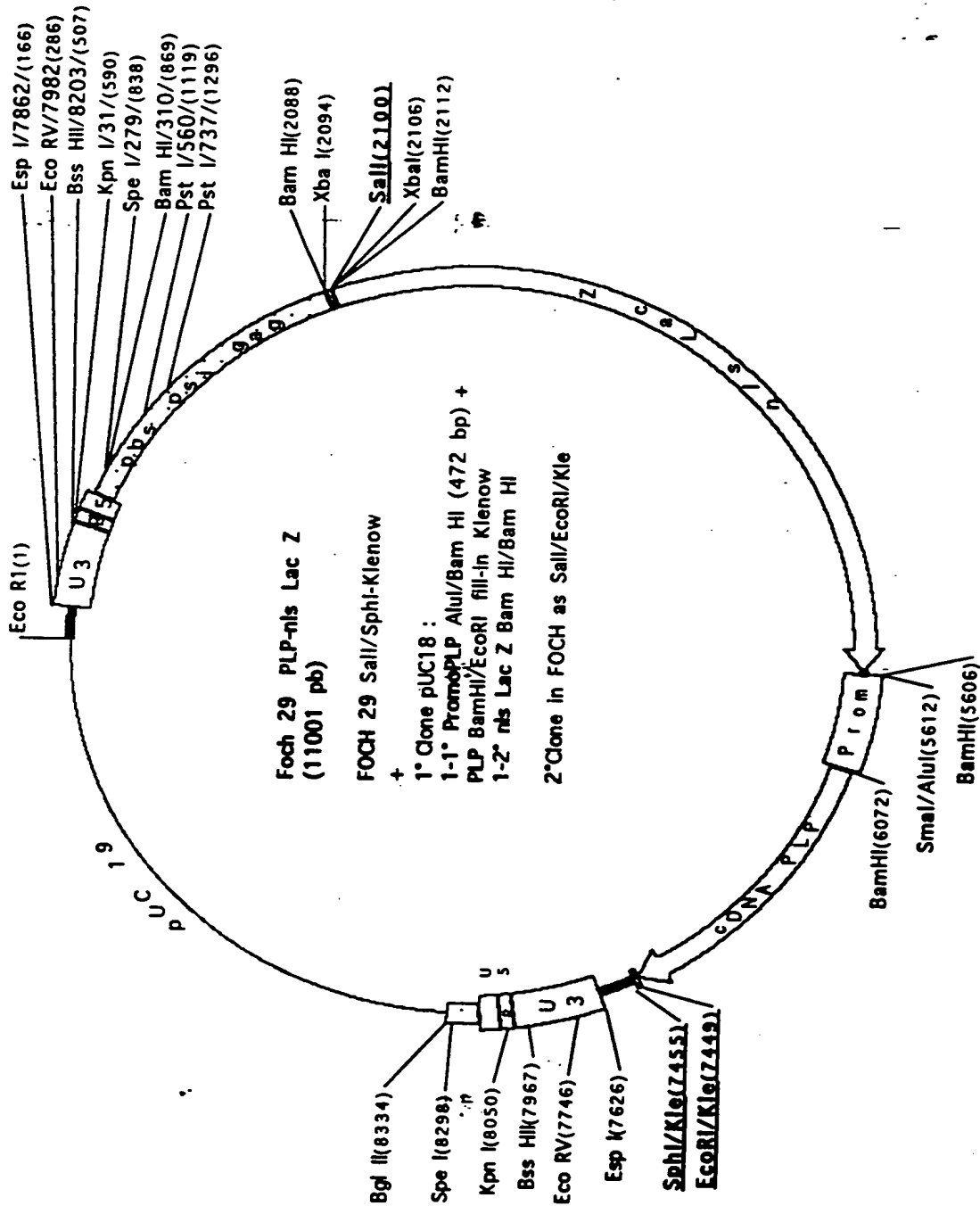


FIGURE 24